

410.018

M. Arand et al

Serial No.: 10/009,030

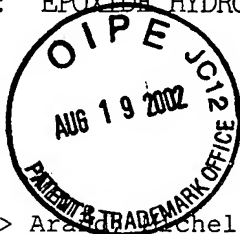
Filed: November 2, 2000

For: EPOXYDE HYDROLASES OF ASPERGILLUS ORIGIN

PTO/PST Rec'd

19 AUG 2002

HS



SEQUENCE LISTING

<110> Archel Michel

Archelas, Alain Robert

Baratti, Jacques

Furstoss, Roland

<120> PROTEINS WITH FUNGICIDAL ORIGIN AND DERIVATIVES, THEIR  
PROCESS OF OBTENTION, AND THEIR USES, NAMELY FOR THE  
PREPARATION OF ENANTIOMERICALLY PURE MOLECULES

<130> 410.018

<140> 10/009,030

<141> 2001-01-11

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1197

<212> DNA

<213> Aspergillus niger

<220>

<221> CDS

<222> (1)..(1197)

Nucleotic Sequence SEQ ID NO : 1

<400> 1

```
atg tcc gct ccg ttc gcc aag ttt ccc tcg tcg gcg agc att tcg cct 48
Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
  1          5          10          15

aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96
Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gin Leu Asp Asp Leu Lys
      20          25          30

acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
      35          40          45

caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192
Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
      50          55          60

cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
      65          70          75          80
```

ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att	288
Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile	
85 90 95	
cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca	336
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala	
100 105 110	
ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg	384
Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu	
115 120 125	
cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg	432
Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu	
130 135 140	
gtt qtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
145 150 155 160	
gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg	528
Asp Lys Asp Phe Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
165 170 175	
atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat	576
Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
180 185 190	
att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
195 200 205	
aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc	672
Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
210 215 220	
ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
225 230 235 240	
atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt	768
Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser	
245 250 255	
act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca	816
Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala	
260 265 270	
tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc	864
Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
275 280 285	
ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr	
290 295 300	

gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act 960  
 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr  
 305 310 315 320

gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008  
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
 325 330 335

cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg 1056  
 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val  
 340 345 350

cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104  
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
 355 360 365

cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152  
 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
 370 375 380

aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197  
 Lys Thr Asp Leu Thr Ala Phe Val Glu Gin Val Trp Gin Lys  
 385 390 395

Peptide Sequence SEQ ID NO : 2

<210> 2

<211> 399

<212>

<213> *Aspergillus niger*

<400> 2

Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro  
 1 5 10 15

Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gin Leu Asp Asp Leu Lys  
 20 25 30

Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
 35 40 45

Gin Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
 50 55 60

Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

Leu Asn Ser Phe Pro Gin Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

---

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

Gin Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu  
 130 135 140

Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu  
 145 150 155 160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gin Leu  
 165 170 175

Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gin Gly Gly Asp  
 180 185 190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205

Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220

Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240

Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser  
 245 250 255

Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala  
 260 265 270

Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro  
 275 280 285

Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr  
 290 295 300

Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr  
 305 310 315 320

Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
 325 330 335

His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val  
 340 345 350

Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
 355 360 365

His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
 370 375 380

Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys  
 385 390 395